

SEQUENCE LISTING

<110> Zhou, Qun-Yong  
Ehlert, Frederick J.

<120> Methods For Modulating Angiogenesis  
Using Prokineticin Receptor Antagonists

<130> 66778-359

<150> US 60/426,203

<151> 2002-11-13

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<151> 2001-11-01

<150> US 60/245,882

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<160> 39

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<211> 1377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55)...(369)

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Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val Ser  
5 10 15

gac tgt gct gtg atc aca ggg gcc tgt gag cgg gat gtc cag tgt ggg 153  
Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly  
20 25 30

gca ggc acc tgc tgt gcc atc agc ctg tgg ctt cga ggg ctg cgg atg 201  
Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met  
35 40 45

tgc acc ccg ctg ggg cgg gaa ggc gag gag tgc cac ccc ggc agc cac 249  
Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His

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50                               55                               60                               65

aag gtc ccc ttc ttc agg aaa cgc aag cac cac acc tgt cct tgc ttg 297
Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu
                               70                               75                               80

ccc aac ctg ctg tgc tcc agg ttc ccg gac ggc agg tac cgc tgc tcc 345
Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser
                               85                               90                               95

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Met Asp Leu Lys Asn Ile Asn Phe
    100                               105

catccttttc tgagcacagc ctggattttt atttctgcca tgaaaccag ctcccatgac 459
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<213> Homo sapiens

<400> 2
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          20          25          30
Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
          35          40          45
Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
          50          55          60
His Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
          65          70          75          80
Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys
          85          90          95
Ser Met Asp Leu Lys Asn Ile Asn Phe
    100                               105
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<210> 3  
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 <212> PRT  
 <213> Homo sapiens

<400> 3  
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 1 5 10 15  
 Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr  
 20 25 30  
 Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val  
 35 40 45  
 Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn  
 50 55 60  
 Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp  
 65 70 75 80  
 Leu Lys Asn Ile Asn Phe  
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<210> 4  
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<220>  
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 <222> (10)...(333)

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 ctg ccg ccg ctg ctg ctc acg ccc cgc gct ggg gac gcc gcc gtg atc 99  
 Leu Pro Pro Leu Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile  
 15 20 25 30  
 acc ggg gct tgt gac aag gac tcc caa tgt ggt gga ggc atg tgc tgt 147  
 Thr Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys  
 35 40 45  
 gct gtc agt atc tgg gtc aag agc ata agg att tgc aca cct atg ggc 195  
 Ala Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly  
 50 55 60  
 aaa ctg gga gac agc tgc cat cca ctg act cgt aaa gtt cca ttt ttt 243  
 Lys Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe  
 65 70 75  
 ggg cgg agg atg cat cac act tgc cca tgt ctg cca ggc ttg gcc tgt 291  
 Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys

80	85	90	
tta cgg act tca ttt aac cga ttt att tgt tta gcc caa aag			333
Leu Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys			
95	100	105	

taatcgctct	ggagtagaaa	ccaaatgtga	atagccacat	cttacctgta	aagtcttact	393
tgtgattgtg	ccaaacaaaa	aatgtgccag	aaagaaatgc	tcttgcttcc	tcaactttcc	453
aagtaacatt	tttatctttg	atttgtaa	gatttttttt	ttttttttta	tcgaaagaga	513
attttacttt	tggatagaaa	tatgaagtgt	aaggcattat	ggaactgggt	cttatttccc	573
tgtttgtgtt	ttggtttgat	ttggcttttt	tcttaa	aatgt	caaaaacgta	633
caaaaatgag	gaaaataaga	atttgatatt	ttgttagaaa	aaactttttt	tttttttctc	693
accaccccaa	gccccatttg	tgccctgccg	cacaaataca	cctacagctt	ttgggtccctt	753
gcctcttcca	cctcaaagaa	tttcaaggct	cttaccttac	tttatttttg	tccatttctc	813
ttccctctct	ttgcatttta	aagtggagg	tttgtctctt	tgagtttgat	ggcagaatca	873
ctgatgggaa	tccagctttt	tgctggcatt	taaatagtga	aaagagtgtg	tatgtgaact	933
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cctgtcactc	aagaggactt	cagctctgct	gttgggctgg	tgtgtggaca	gaaggaatgg	1053
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catttacttc	ttttactttt	tataaagttt	tttttcctta	gtctcctact	tagagatatt	1173
ctagaaaatg	tcacttgaag	aggaagtatt	tattttaatc	tggcacaaca	ctaattacca	1233
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<210> 5  
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 <213> Homo sapiens

<400> 5
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Pro Leu Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile Thr Gly
20 25 30
Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala Val
35 40 45
Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu
50 55 60
Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe Gly Arg
65 70 75 80
Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu Arg
85 90 95
Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys
100 105

<210> 6  
 <211> 81  
 <212> PRT  
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<400> 6

Ala Val Ile Thr Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly  
1 5 10 15  
Met Cys Cys Ala Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr  
20 25 30  
Pro Met Gly Lys Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val  
35 40 45  
Pro Phe Phe Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly  
50 55 60  
Leu Ala Cys Leu Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln  
65 70 75 80  
Lys

<210> 7  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 7  
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1 5 10 15  
Lys Arg Lys Lys Glu  
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<210> 8  
<211> 21  
<212> PRT  
<213> Homo sapiens

<400> 8  
Ser His Val Ala Asn Gly Arg Gln Glu Arg Arg Arg Ala Lys Arg Arg  
1 5 10 15  
Lys Arg Lys Lys Glu  
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<210> 9  
<211> 19  
<212> PRT  
<213> Homo sapiens

<400> 9  
Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val  
1 5 10 15  
Ser Asp Cys

<210> 10  
<211> 26  
<212> PRT

<213> Homo sapiens

<400> 10

Met Arg Ser Leu Cys Cys Ala Pro Leu Leu Leu Leu Leu Leu Pro  
1 5 10 15  
Leu Leu Leu Thr Pro Pro Ala Gly Asp Ala  
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<210> 11

<211> 96

<212> PRT

<213> Bombina variegata

<400> 11

Met Lys Cys Phe Ala Gln Ile Val Val Leu Leu Leu Val Ile Ala Phe  
1 5 10 15  
Ser His Gly Ala Val Ile Thr Gly Ala Cys Asp Lys Asp Val Gln Cys  
20 25 30  
Gly Ser Gly Thr Cys Cys Ala Ala Ser Ala Trp Ser Arg Asn Ile Arg  
35 40 45  
Phe Cys Ile Pro Leu Gly Asn Ser Gly Glu Asp Cys His Pro Ala Ser  
50 55 60  
His Lys Val Pro Tyr Asp Gly Lys Arg Leu Ser Ser Leu Cys Pro Cys  
65 70 75 80  
Lys Ser Gly Leu Thr Cys Ser Lys Ser Gly Glu Lys Phe Lys Cys Ser  
85 90 95

<210> 12

<211> 81

<212> PRT

<213> Dendroaspis polylepis polylepis

<400> 12

Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Leu Gln Cys Gly Lys Gly  
1 5 10 15  
Thr Cys Cys Ala Val Ser Leu Trp Ile Lys Ser Val Arg Val Cys Thr  
20 25 30  
Pro Val Gly Thr Ser Gly Glu Asp Cys His Pro Ala Ser His Lys Ile  
35 40 45  
Pro Phe Ser Gly Gln Arg Lys Met His His Thr Cys Pro Cys Ala Pro  
50 55 60  
Asn Leu Ala Cys Val Gln Thr Ser Pro Lys Lys Phe Lys Cys Leu Ser  
65 70 75 80  
Lys

<210> 13

<211> 81

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 13

Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val	Gln	Cys	Gly	Ala	Gly
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Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg	Gly	Leu	Arg	Met	Cys	Thr
			20					25					30		
Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys	His	Pro	Gly	Ser	His	Lys	Val
		35				40					45				
Pro	Phe	Phe	Gly	Arg	Arg	Met	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Gly
	50					55				60					
Leu	Ala	Cys	Leu	Arg	Thr	Ser	Phe	Asn	Arg	Phe	Ile	Cys	Leu	Ala	Gln
65					70					75					80
Lys															

<210> 14

<211> 86

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 14

Ala	Val	Ile	Thr	Gly	Ala	Cys	Asp	Lys	Asp	Ser	Gln	Cys	Gly	Gly	Gly
1				5					10					15	
Met	Cys	Cys	Ala	Val	Ser	Ile	Trp	Val	Lys	Ser	Ile	Arg	Ile	Cys	Thr
			20					25					30		
Pro	Met	Gly	Lys	Leu	Gly	Asp	Ser	Cys	His	Pro	Leu	Thr	Arg	Lys	Val
		35				40					45				
Pro	Phe	Phe	Arg	Lys	Arg	Lys	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Asn
	50					55				60					
Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys	Ser	Met	Asp
65					70					75					80
Leu	Lys	Asn	Ile	Asn	Phe										
				85											

<210> 15

<211> 89

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 15

Gly	Ile	Leu	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val	Gln	Cys
1				5					10					15	

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Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
      20                      25                      30
Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
      35                      40                      45
His Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
      50                      55                      60
Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys
65                      70                      75                      80
Ser Met Asp Leu Lys Asn Ile Asn Phe
      85

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<210> 16  
 <211> 85  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic construct

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<400> 16
Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly Thr
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Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr Pro
      20                      25                      30
Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val Pro
      35                      40                      45
Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn Leu
 50                      55                      60
Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp Leu
65                      70                      75                      80
Lys Asn Ile Asn Phe
      85

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<210> 17  
 <211> 86  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthetic construct

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<400> 17
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 1                      5                      10                      15
Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr
      20                      25                      30
Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val
      35                      40                      45
Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn
 50                      55                      60
Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp

```



```

65          70          75          80
Leu Lys Asn Ile Asn Phe
          85

```

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<210> 18
<211> 87
<212> PRT
<213> Artificial Sequence
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<220>  
<223> synthetic construct

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<400> 18
Met Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala
 1                    5                      10                15
Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys
                20                      25                30
Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys
                35                      40                45
Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro
                50                      55                60
Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met
65                    70                      75                80
Asp Leu Lys Asn Ile Asn Phe
                85

```

```
<210> 19
<211> 14
<212> PRT
<213> Artificial Sequence
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<220>  
<223> synthetic construct

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<400> 19
Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly
  1                   5                   10
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<210> 20
<211> 86
<212> PRT
<213> Homo sapiens
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<400> 20  
Met Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly  
1 5 10 15  
Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr  
20 25 30  
Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val  
35 40 45

Pro	Phe	Phe	Arg	Lys	Arg	Lys	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Asn
	50					55					60				
Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys	Ser	Met	Asp
65					70					75					80
Leu	Lys	Asn	Ile	Asn	Phe										
				85											

<210> 21  
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 <212> PRT  
 <213> Homo sapiens

<400> 21  
 Ala Val Ile Thr Gly Ala  
 1 5

<210> 22  
 <211> 5  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Val Ile Thr Gly Ala  
 1 5

<210> 23  
 <211> 7  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Met Ala Val Ile Thr Gly Ala  
 1 5

<210> 24  
 <211> 393  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
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 1 5 10 15  
 Thr Ser Phe Leu Ser Val Leu Asn Pro His Gly Ala His Ala Thr Ser  
 20 25 30  
 Phe Pro Phe Asn Phe Ser Tyr Ser Asp Tyr Asp Met Pro Leu Asp Glu  
 35 40 45  
 Asp Glu Asp Val Thr Asn Ser Arg Thr Phe Phe Ala Ala Lys Ile Val  
 50 55 60  
 Ile Gly Met Ala Leu Val Gly Ile Met Leu Val Cys Gly Ile Gly Asn

65				70					75				80		
Phe	Ile	Phe	Ile	Ala	Ala	Leu	Val	Arg	Tyr	Lys	Lys	Leu	Arg	Asn	Leu
				85					90					95	
Thr	Asn	Leu	Leu	Ile	Ala	Asn	Leu	Ala	Ile	Ser	Asp	Phe	Leu	Val	Ala
			100					105					110		
Ile	Val	Cys	Cys	Pro	Phe	Glu	Met	Asp	Tyr	Tyr	Val	Val	Arg	Gln	Leu
		115					120					125			
Ser	Trp	Glu	His	Gly	His	Val	Leu	Cys	Thr	Ser	Val	Asn	Tyr	Leu	Arg
	130					135					140				
Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn	Ala	Leu	Leu	Ala	Ile	Ala	Ile
145					150				155					160	
Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	Leu	Arg	Pro	Arg	Met	Lys	Cys
				165					170					175	
Gln	Thr	Ala	Thr	Gly	Leu	Ile	Ala	Leu	Val	Trp	Thr	Val	Ser	Ile	Leu
			180					185					190		
Ile	Ala	Ile	Pro	Ser	Ala	Tyr	Phe	Thr	Thr	Glu	Thr	Val	Leu	Val	Ile
	195						200					205			
Val	Lys	Ser	Gln	Glu	Lys	Ile	Phe	Cys	Gly	Gln	Ile	Trp	Pro	Val	Asp
	210					215					220				
Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe	Leu	Phe	Ile	Phe	Gly	Ile	Glu
225					230				235					240	
Phe	Val	Gly	Pro	Val	Val	Thr	Met	Thr	Leu	Cys	Tyr	Ala	Arg	Met	Thr
				245					250					255	
Arg	Glu	Leu	Trp	Phe	Lys	Ala	Val	Pro	Gly	Phe	Gln	Thr	Glu	Gln	Ile
		260						265					270		
Arg	Lys	Arg	Leu	Arg	Cys	Arg	Arg	Lys	Thr	Val	Leu	Val	Leu	Met	Cys
	275					280						285			
Ile	Leu	Thr	Ala	Tyr	Val	Leu	Cys	Trp	Ala	Pro	Phe	Tyr	Gly	Phe	Thr
	290					295					300				
Ile	Val	Arg	Asp	Phe	Phe	Pro	Thr	Val	Phe	Val	Lys	Glu	Lys	His	Tyr
305					310				315					320	
Leu	Thr	Ala	Phe	Tyr	Ile	Val	Glu	Cys	Ile	Ala	Met	Ser	Asn	Ser	Met
				325					330					335	
Ile	Asn	Thr	Leu	Cys	Phe	Val	Thr	Val	Lys	Asn	Asp	Thr	Val	Lys	Tyr
		340						345					350		
Phe	Lys	Lys	Ile	Met	Leu	Leu	His	Trp	Lys	Ala	Ser	Tyr	Asn	Gly	Gly
	355					360						365			
Lys	Ser	Ser	Ala	Asp	Leu	Asp	Leu	Lys	Thr	Ile	Gly	Met	Pro	Ala	Thr
	370					375					380				
Glu	Glu	Val	Asp	Cys	Ile	Arg	Leu	Lys							
385					390										

<210> 25  
 <211> 384  
 <212> PRT  
 <213> Homo sapiens

<400> 25  
 Met Ala Ala Gln Asn Gly Asn Thr Ser Phe Thr Pro Asn Phe Asn Pro  
 1 5 10 15  
 Pro Gln Asp His Ala Ser Ser Leu Ser Phe Asn Phe Ser Tyr Gly Asp  
 20 25 30

Tyr	Asp	Leu	Pro	Met	Asp	Glu	Asp	Glu	Asp	Met	Thr	Lys	Thr	Arg	Thr
	35						40					45			
Phe	Phe	Ala	Ala	Lys	Ile	Val	Ile	Gly	Ile	Ala	Leu	Ala	Gly	Ile	Met
	50					55					60				
Leu	Val	Cys	Gly	Ile	Gly	Asn	Phe	Val	Phe	Ile	Ala	Ala	Leu	Thr	Arg
65					70					75					80
Tyr	Lys	Lys	Leu	Arg	Asn	Leu	Thr	Asn	Leu	Leu	Ile	Ala	Asn	Leu	Ala
				85					90					95	
Ile	Ser	Asp	Phe	Leu	Val	Ala	Ile	Ile	Cys	Cys	Pro	Phe	Glu	Met	Asp
			100					105					110		
Tyr	Tyr	Val	Val	Arg	Gln	Leu	Ser	Trp	Glu	His	Gly	His	Val	Leu	Cys
	115						120				125				
Ala	Ser	Val	Asn	Tyr	Leu	Arg	Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn
	130					135					140				
Ala	Leu	Leu	Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro
145					150					155					160
Leu	Lys	Pro	Arg	Met	Asn	Tyr	Gln	Thr	Ala	Ser	Phe	Leu	Ile	Ala	Leu
				165					170					175	
Val	Trp	Met	Val	Ser	Ile	Leu	Ile	Ala	Ile	Pro	Ser	Ala	Tyr	Phe	Ala
			180					185					190		
Thr	Glu	Thr	Val	Leu	Phe	Ile	Val	Lys	Ser	Gln	Glu	Lys	Ile	Phe	Cys
	195						200					205			
Gly	Gln	Ile	Trp	Pro	Val	Asp	Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe
	210					215					220				
Leu	Phe	Ile	Phe	Gly	Val	Glu	Phe	Val	Gly	Pro	Val	Val	Thr	Met	Thr
225					230					235					240
Leu	Cys	Tyr	Ala	Arg	Ile	Ser	Arg	Glu	Leu	Trp	Phe	Lys	Ala	Val	Pro
				245					250					255	
Gly	Phe	Gln	Thr	Glu	Gln	Ile	Arg	Lys	Arg	Leu	Arg	Cys	Arg	Arg	Lys
			260					265					270		
Thr	Val	Leu	Val	Leu	Met	Cys	Ile	Leu	Thr	Ala	Tyr	Val	Leu	Cys	Trp
		275					280					285			
Ala	Pro	Phe	Tyr	Gly	Phe	Thr	Ile	Val	Arg	Asp	Phe	Phe	Pro	Thr	Val
	290					295					300				
Phe	Val	Lys	Glu	Lys	His	Tyr	Leu	Thr	Ala	Phe	Tyr	Val	Val	Glu	Cys
305					310					315					320
Ile	Ala	Met	Ser	Asn	Ser	Met	Ile	Asn	Thr	Val	Cys	Phe	Val	Thr	Val
				325					330					335	
Lys	Asn	Asn	Thr	Met	Lys	Tyr	Phe	Lys	Lys	Met	Met	Leu	Leu	His	Trp
			340					345					350		
Arg	Pro	Ser	Gln	Arg	Gly	Ser	Lys	Ser	Ser	Ala	Asp	Leu	Asp	Leu	Arg
		355					360					365			
Thr	Asn	Gly	Val	Pro	Thr	Thr	Glu	Glu	Val	Asp	Cys	Ile	Arg	Leu	Lys
	370					375					380				

<210> 26  
 <211> 393  
 <212> PRT  
 <213> Mus musculus

<400> 26  
 Met Glu Thr Thr Val Gly Ala Leu Gly Glu Asn Thr Thr Asp Thr Phe

1		5		10		15
Thr	Asp	Phe	Phe	Ser	Ala	Leu
		20				
Leu	Pro	Phe	Thr	Phe	Ser	Tyr
		35				
Glu	Glu	Asp	Val	Thr	Asn	Ser
		50				
Ile	Gly	Met	Ala	Leu	Val	Gly
65				70		
Phe	Ile	Phe	Ile	Thr	Ala	Leu
				85		
Thr	Asn	Leu	Leu	Ile	Ala	Asn
		100				
Ile	Val	Cys	Cys	Pro	Phe	Glu
		115				
Ser	Trp	Glu	His	Gly	His	Val
		130				
Thr	Val	Ser	Leu	Tyr	Val	Ser
145				150		
Asp	Arg	Tyr	Leu	Ala	Ile	Val
				165		
Gln	Thr	Ala	Ala	Gly	Leu	Ile
		180				
Ile	Ala	Ile	Pro	Ala	Ala	Tyr
		195				
Val	Glu	Arg	Gln	Glu	Lys	Ile
		210				
Gln	Gln	Phe	Tyr	Tyr	Arg	Ser
225				230		
Phe	Val	Gly	Pro	Val	Val	Ala
				245		
Arg	Glu	Leu	Trp	Phe	Lys	Ala
		260				
Arg	Arg	Thr	Val	Arg	Cys	Arg
		275				
Val	Leu	Ser	Ala	Tyr	Val	Leu
		290				
Ile	Val	Arg	Asp	Phe	Phe	Pro
305				310		
Leu	Thr	Ala	Phe	Tyr	Val	Val
				325		
Ile	Asn	Thr	Leu	Cys	Phe	Val
		340				
Leu	Lys	Arg	Ile	Leu	Arg	Leu
		355				
Lys	Ala	Ser	Ala	Asp	Leu	Asp
		370				
Glu	Glu	Val	Asp	Cys	Ile	Arg
385						

<210> 27

<211> 381

<212> PRT

<213> Mus musculus

<400> 27

Met	Gly	Pro	Gln	Asn	Arg	Asn	Thr	Ser	Phe	Ala	Pro	Asp	Leu	Asn	Pro
1				5					10					15	
Pro	Gln	Asp	His	Val	Ser	Leu	Asn	Tyr	Ser	Tyr	Gly	Asp	Tyr	Asp	Leu
			20					25					30		
Pro	Leu	Gly	Glu	Asp	Glu	Asp	Val	Thr	Lys	Thr	Gln	Thr	Phe	Phe	Ala
		35					40					45			
Ala	Lys	Ile	Val	Ile	Gly	Val	Ala	Leu	Ala	Gly	Ile	Met	Leu	Val	Cys
	50					55					60				
Gly	Ile	Gly	Asn	Phe	Val	Phe	Ile	Ala	Ala	Leu	Ala	Arg	Tyr	Lys	Lys
65					70					75				80	
Leu	Arg	Asn	Leu	Thr	Asn	Leu	Leu	Ile	Ala	Asn	Leu	Ala	Ile	Ser	Asp
				85					90					95	
Phe	Leu	Val	Ala	Ile	Val	Cys	Cys	Pro	Phe	Glu	Met	Asp	Tyr	Tyr	Val
			100					105					110		
Val	Arg	Gln	Leu	Ser	Trp	Ala	His	Gly	His	Val	Leu	Cys	Ala	Ser	Val
		115					120					125			
Asn	Tyr	Leu	Arg	Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn	Ala	Leu	Leu
	130					135					140				
Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	Leu	Lys	Pro
145					150					155				160	
Arg	Met	Asn	Tyr	Gln	Thr	Ala	Ser	Phe	Leu	Ile	Ala	Leu	Val	Trp	Met
				165					170					175	
Val	Ser	Ile	Leu	Ile	Ala	Val	Pro	Ser	Ala	Tyr	Phe	Thr	Thr	Glu	Thr
			180					185					190		
Ile	Leu	Val	Ile	Val	Lys	Asn	Gln	Glu	Lys	Ile	Phe	Cys	Gly	Gln	Ile
	195					200						205			
Trp	Ser	Val	Asp	Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe	Leu	Phe	Val
	210					215					220				
Phe	Gly	Leu	Glu	Phe	Val	Gly	Pro	Val	Val	Thr	Met	Thr	Leu	Cys	Tyr
225					230					235				240	
Ala	Arg	Ile	Ser	Gln	Glu	Leu	Trp	Phe	Lys	Ala	Val	Pro	Gly	Phe	Gln
				245					250					255	
Thr	Glu	Gln	Ile	Arg	Lys	Arg	Leu	Arg	Cys	Arg	Arg	Lys	Thr	Val	Leu
			260				265						270		
Leu	Leu	Met	Gly	Ile	Leu	Thr	Ala	Tyr	Val	Leu	Cys	Trp	Ala	Pro	Phe
	275					280					285				
Tyr	Gly	Phe	Thr	Ile	Val	Arg	Asp	Phe	Phe	Pro	Thr	Val	Val	Val	Lys
	290					295				300					
Glu	Lys	His	Tyr	Leu	Thr	Ala	Phe	Tyr	Val	Val	Glu	Cys	Ile	Ala	Met
305					310					315				320	
Ser	Asn	Ser	Met	Ile	Asn	Thr	Ile	Cys	Phe	Val	Thr	Val	Lys	Asn	Asn
				325					330					335	
Thr	Met	Lys	Tyr	Phe	Lys	Lys	Met	Leu	Arg	Leu	His	Trp	Arg	Pro	Ser
			340				345						350		
His	Tyr	Gly	Ser	Lys	Ser	Ser	Ala	Asp	Leu	Asp	Leu	Lys	Thr	Ser	Gly
	355						360					365			
Val	Pro	Ala	Thr	Glu	Glu	Val	Asp	Cys	Ile	Arg	Leu	Lys			
	370					375					380				

<210> 28  
<211> 86  
<212> PRT  
<213> Mus musculus

<400> 28  
Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Ile Gln Cys Gly Ala Gly  
1 5 10 15  
Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Leu Cys Thr  
20 25 30  
Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Ile  
35 40 45  
Pro Phe Leu Arg Lys Arg Gln His His Thr Cys Pro Cys Ser Pro Ser  
50 55 60  
Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Phe Arg Asp  
65 70 75 80  
Leu Lys Asn Ala Asn Phe  
85

<210> 29  
<211> 81  
<212> PRT  
<213> Mus musculus

<400> 29  
Ala Val Ile Thr Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly  
1 5 10 15  
Met Cys Cys Ala Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr  
20 25 30  
Pro Met Gly Gln Val Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val  
35 40 45  
Pro Phe Trp Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly  
50 55 60  
Leu Ala Cys Leu Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Arg  
65 70 75 80  
Lys

<210> 30  
<211> 86  
<212> PRT  
<213> Rattus sp.

<400> 30  
Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly  
1 5 10 15  
Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Leu Cys Thr  
20 25 30  
Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Ile  
35 40 45

Pro	Phe	Phe	Arg	Lys	Arg	Gln	His	His	Thr	Cys	Pro	Cys	Ser	Pro	Ser
50						55					60				
Leu	Leu	Cys	Ser	Arg	Phe	Pro	Asp	Gly	Arg	Tyr	Arg	Cys	Ser	Gln	Asp
65					70					75					80
Leu	Lys	Asn	Val	Asn	Phe										
				85											

<210> 31  
 <211> 81  
 <212> PRT  
 <213> Rattus sp.

Ala	Val	Ile	Thr	Gly	Ala	Cys	Asp	Lys	Asp	Ser	Gln	Cys	Gly	Gly	Gly
1				5					10					15	
Met	Cys	Cys	Ala	Val	Ser	Ile	Trp	Val	Lys	Ser	Ile	Arg	Ile	Cys	Thr
			20					25					30		
Pro	Met	Gly	Gln	Val	Gly	Asp	Ser	Cys	His	Pro	Leu	Thr	Arg	Lys	Val
		35				40						45			
Pro	Phe	Trp	Gly	Arg	Arg	Met	His	His	Thr	Cys	Pro	Cys	Leu	Pro	Gly
	50					55				60					
Leu	Ala	Cys	Leu	Arg	Thr	Ser	Phe	Asn	Arg	Phe	Ile	Cys	Leu	Ala	Arg
65					70					75					80
Lys															

<210> 32  
 <211> 77  
 <212> PRT  
 <213> Bombina maxima

Ala	Val	Ile	Thr	Gly	Ala	Cys	Asp	Arg	Asp	Val	Gln	Cys	Gly	Ser	Gly
1				5					10					15	
Thr	Cys	Cys	Ala	Ala	Ser	Leu	Trp	Ser	Arg	Asn	Ile	Arg	Phe	Cys	Val
			20					25					30		
Pro	Leu	Gly	Asn	Asn	Gly	Glu	Glu	Cys	His	Pro	Ala	Ser	His	Lys	Val
		35				40						45			
Pro	Tyr	Asn	Gly	Lys	Arg	Leu	Ser	Ser	Leu	Cys	Pro	Cys	Lys	Ser	Gly
	50					55				60					
Leu	Thr	Cys	Ser	Lys	Ser	Gly	Glu	Lys	Phe	Gln	Cys	Ser			
65					70					75					

<210> 33  
 <211> 1204  
 <212> DNA  
 <213> Macaca mulatta

<220>  
 <221> CDS



<222> (5)...(329)

<400> 33

cgcc atg agg agc ctg tgc tgc gcc cca ctc ctg ctc ctc ctg ctg ctg	49
Met Arg Ser Leu Cys Cys Ala Pro Leu Leu Leu Leu Leu Leu Leu	
1 5 10 15	

ccg ccg ctg ctg ctc acg ccc cgc gtc ggg gac gcc gcc gtg atc acc	97
Pro Pro Leu Leu Leu Thr Pro Arg Val Gly Asp Ala Ala Val Ile Thr	
20 25 30	

ggg gct tgt gac aag gac tcc caa tgt ggt gga ggc atg tgc tgt gct	145
Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala	
35 40 45	

gtc agt atc tgg gtt aag agc ata agg att tgc aca cct atg ggc aaa	193
Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys	
50 55 60	

ctg gga gac agc tgc cat cca ctg act cgt aaa gtt cca ttt gtt ggg	241
Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Val Gly	
65 70 75	

cgg agg atg cat cac act tgc cca tgt ctg cca ggc ttg gcc tgt tta	289
Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu	
80 85 90 95	

cgg act tca ttt aac cga ttt att tgt tta gcc cga aag t aatcgcttta	339
Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Arg Lys	
100 105	

aagtagaaac caaatgtgaa tagccacatc ttatctgtaa agtcttactt gtgattgtgc	399
caaacaaaaa atgtgccaga aagaaatgct tttgcttcct caactttcca agtaactttt	459
ttatctttga gttttaaatg attttttttt taatcgggaa ttttactttt ggatagaaat	519
ataaagtgtg aggcattgtg gaactgggtc tcatttccct gtttgtgttt tggtttggtt	579
tggctttttt cttaaagtgc aaaaacatac ccattttcac aaaaatgagg aaaataggaa	639
tttgatattt tgtagagaa actttttttt tcctcaccat cccaagcccc atttgtgccc	699
cgccacacca taccatacat acatacatac atacatacat acatacatac aacttttggt	759
cccttgcttc ttccacctca aagaatttca aggcccttac cttactttat tttctccat	819
ttctcttccc tgctcttgca ttttaaagtg gtaggtttat ctctttgagt ttgatggcag	879
aatcgctgat gggaatccag ctttttgccg gctattttaa tagtgaaaag agtttatatg	939
tgaacttgac actccaaact cctctcatgg cgtggacgct gggagtgtg ccggaccctt	999
cctaaacctg tcaactcaaga ggacttcggc tctgctgttg ggctgggtgtg tggacagaag	1059
gaatggaaag ctaaattaat ttagtcaga tttctaggtt tgggtttttc taaaaatgaa	1119
agattacgtt tactttcttt tctttttata aagttttttt ttcttagtct cctacttaga	1179
gatattctag aaaatgtcac ttgaa	1204

<210> 34

<211> 108

<212> PRT

<213> Macaca mulatta

<400> 34

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Met Arg Ser Leu Cys Cys Ala Pro Leu Leu Leu Leu Leu Leu Pro
 1          5          10          15
Pro Leu Leu Leu Thr Pro Arg Val Gly Asp Ala Ala Val Ile Thr Gly
          20          25          30
Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala Val
          35          40          45
Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu
          50          55          60
Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Val Gly Arg
65          70          75          80
Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu Arg
          85          90          95
Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Arg Lys
          100          105

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<210> 35  
 <211> 1155  
 <212> DNA  
 <213> Pan troglodyte

<220>  
 <221> CDS  
 <222> (1)...(1155)

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<400> 35
atg gca gcc cag aat gga aac acc agt ttc gca ccc aac ttt aat cca      48
Met Ala Ala Gln Asn Gly Asn Thr Ser Phe Ala Pro Asn Phe Asn Pro
 1          5          10          15

ccg caa gac cat gcc tcc tcc ctc tcc ttt aac ttc agt tat ggt gat      96
Pro Gln Asp His Ala Ser Ser Leu Ser Phe Asn Phe Ser Tyr Gly Asp
          20          25          30

tat gac ctc cct atg gat gag gat gag gac atg acc aag acc cgg acc      144
Tyr Asp Leu Pro Met Asp Glu Asp Glu Asp Met Thr Lys Thr Arg Thr
          35          40          45

ttc ctc gca gcc aag atc gtc gtt ggc att gca ctg gca ggc atc atg      192
Phe Leu Ala Ala Lys Ile Val Val Gly Ile Ala Leu Ala Gly Ile Met
          50          55          60

ctg gtc tgc ggc atc ggt aac ttt gtc ttt atc gct gcc ctc acc cgc      240
Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg
          65          70          75          80

tat aag aag ttg cgc aac ctc acc aat ctg ctc att gcc aac ctg gcc      288
Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala
          85          90          95

atc tcc gac ttc ctg gtg gcc atc atc tgc tgc ccc ttc gag atg gac      336
Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp
          100          105          110

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tac tac gtg gta cgg cag ctc tcc tgg gag cat ggc cac gtg ctc tgt	384
Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys	
115 120 125	
gcc tcc gtc aac tac ctg cgc acc gtc tcc ctc tac gtc tcc acc aat	432
Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn	
130 135 140	
gcc ttg ctg gcc atc gcc att gac aga tat ctc gcc att gtt cac cct	480
Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro	
145 150 155 160	
ttg aaa cca cgg atg aat tat caa acg gcc tcc ttc ctg atc gcc ttg	528
Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu	
165 170 175	
gtc tgg atg gtg tcc att ctc att gcc atc cca tcg gcc tac ttt gca	576
Val Trp Met Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala	
180 185 190	
aca gaa acc gtc ctc ttt att gtc aag agc cag gag aag atc ttc tgt	624
Thr Glu Thr Val Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys	
195 200 205	
ggc cag atc tgg ccc gtg gat cag cag ctc tac tac aag tcc tac ttc	672
Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe	
210 215 220	
ctc ttc atc ttt ggt gtc gag ttc gtg ggc cct gtg gtc acc atg acc	720
Leu Phe Ile Phe Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr	
225 230 235 240	
ctg tgc tat gcc agg atc tcc cgg gag ctc tgg ttc aag gca gtc cct	768
Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val Pro	
245 250 255	
ggg ttc cag acg gag cag att cgc aag cgg ctg cgc tgc cgc agg aag	816
Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys	
260 265 270	
acg gtc ctg gtg ctc atg tgc att ctc acg gcc tat gtg ctg tgc tgg	864
Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp	
275 280 285	
gca ccc ttc tac ggt ttc acc atc gtt cgt gac ttc ttc ccc act gtg	912
Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val	
290 295 300	
ttc gtg aag gaa aag cac tac ctc act gcc ttc tac gtg gtc gag tgc	960
Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Val Val Glu Cys	
305 310 315 320	
atc gcc atg agc aac agc atg atc aac acc gtg tgc ttc gtg acg gtc	1008

Ile	Ala	Met	Ser	Asn	Ser	Met	Ile	Asn	Thr	Val	Cys	Phe	Val	Thr	Val		
				325					330					335			
aag	aac	aac	acc	atg	aag	tac	ttc	aag	aag	atg	atg	ctg	ctg	cac	tgg		1056
Lys	Asn	Asn	Thr	Met	Lys	Tyr	Phe	Lys	Lys	Met	Met	Leu	Leu	His	Trp		
			340					345					350				
cg	t	ccc	tcc	cag	cgg	ggg	agc	aag	tcc	agt	gcc	gac	ctt	gac	ctc	aga	1104
Arg	Pro	Ser	Gln	Arg	Gly	Ser	Lys	Ser	Ser	Ala	Asp	Leu	Asp	Leu	Arg		
			355				360					365					
acc	aac	ggg	gtg	ccc	gcc	aca	gaa	gag	gtg	gac	tgt	atc	agg	ctg	aag		1152
Thr	Asn	Gly	Val	Pro	Ala	Thr	Glu	Glu	Val	Asp	Cys	Ile	Arg	Leu	Lys		
			370				375				380						
tga																	1155
*																	

<210> 36  
 <211> 384  
 <212> PRT  
 <213> Pan troglodyte

<400> 36

Met	Ala	Ala	Gln	Asn	Gly	Asn	Thr	Ser	Phe	Ala	Pro	Asn	Phe	Asn	Pro		
1				5					10					15			
Pro	Gln	Asp	His	Ala	Ser	Ser	Leu	Ser	Phe	Asn	Phe	Ser	Tyr	Gly	Asp		
			20					25					30				
Tyr	Asp	Leu	Pro	Met	Asp	Glu	Asp	Glu	Asp	Met	Thr	Lys	Thr	Arg	Thr		
		35				40						45					
Phe	Leu	Ala	Ala	Lys	Ile	Val	Val	Gly	Ile	Ala	Leu	Ala	Gly	Ile	Met		
	50					55					60						
Leu	Val	Cys	Gly	Ile	Gly	Asn	Phe	Val	Phe	Ile	Ala	Ala	Leu	Thr	Arg		
65					70				75						80		
Tyr	Lys	Lys	Leu	Arg	Asn	Leu	Thr	Asn	Leu	Leu	Ile	Ala	Asn	Leu	Ala		
				85				90						95			
Ile	Ser	Asp	Phe	Leu	Val	Ala	Ile	Ile	Cys	Cys	Pro	Phe	Glu	Met	Asp		
		100					105						110				
Tyr	Tyr	Val	Val	Arg	Gln	Leu	Ser	Trp	Glu	His	Gly	His	Val	Leu	Cys		
		115				120						125					
Ala	Ser	Val	Asn	Tyr	Leu	Arg	Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn		
		130				135					140						
Ala	Leu	Leu	Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro		
145				150						155					160		
Leu	Lys	Pro	Arg	Met	Asn	Tyr	Gln	Thr	Ala	Ser	Phe	Leu	Ile	Ala	Leu		
				165				170						175			
Val	Trp	Met	Val	Ser	Ile	Leu	Ile	Ala	Ile	Pro	Ser	Ala	Tyr	Phe	Ala		
		180				185							190				
Thr	Glu	Thr	Val	Leu	Phe	Ile	Val	Lys	Ser	Gln	Glu	Lys	Ile	Phe	Cys		
		195				200					205						
Gly	Gln	Ile	Trp	Pro	Val	Asp	Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe		

210	215	220
Leu Phe Ile Phe Gly Val	Glu Phe Val Gly Pro	Val Val Thr Met Thr
225	230	235
Leu Cys Tyr Ala Arg Ile	Ser Arg Glu Leu Trp	Phe Lys Ala Val Pro
245	250	255
Gly Phe Gln Thr Glu Gln	Ile Arg Lys Arg Leu	Arg Cys Arg Arg Lys
260	265	270
Thr Val Leu Val Leu Met	Cys Ile Leu Thr Ala	Tyr Val Leu Cys Trp
275	280	285
Ala Pro Phe Tyr Gly Phe	Thr Ile Val Arg Asp	Phe Phe Pro Thr Val
290	295	300
Phe Val Lys Glu Lys His	Tyr Leu Thr Ala Phe	Tyr Val Val Glu Cys
305	310	315
Ile Ala Met Ser Asn Ser	Met Ile Asn Thr Val	Cys Phe Val Thr Val
325	330	335
Lys Asn Asn Thr Met Lys	Tyr Phe Lys Lys Met	Met Leu Leu His Trp
340	345	350
Arg Pro Ser Gln Arg Gly	Ser Lys Ser Ser Ala	Asp Leu Asp Leu Arg
355	360	365
Thr Asn Gly Val Pro Ala	Thr Glu Glu Val Asp	Cys Ile Arg Leu Lys
370	375	380

<210> 37  
 <211> 1155  
 <212> DNA  
 <213> Saimiri sciureus

<220>  
 <221> CDS  
 <222> (1)...(1155)

<400> 37	
atg gca gcc cag aat gga aac acc agt ttt gca ccc aac ttt aat cca	48
Met Ala Ala Gln Asn Gly Asn Thr Ser Phe Ala Pro Asn Phe Asn Pro	
1 5 10 15	
ccc caa gac cat gcc tcc tcc ctc tcc ttc aac ttc agt tat ggt gat	96
Pro Gln Asp His Ala Ser Ser Leu Ser Phe Asn Phe Ser Tyr Gly Asp	
20 25 30	
tac gac ctc cct atg gat gag gat gag gac atg acc aag acc cgg acc	144
Tyr Asp Leu Pro Met Asp Glu Asp Glu Asp Met Thr Lys Thr Arg Thr	
35 40 45	
ttc ttt gca gcc aag att gtc atc ggc att gca ctg gca ggc atc atg	192
Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met	
50 55 60	
ctg gtc tgt ggt gtc ggt aac ttt gtc ttt atc gct gcc ctc acc cgc	240
Leu Val Cys Gly Val Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg	
65 70 75 80	
tat aag aag ctg cgc aac ctc acc aat ctg ctc att gcc aac ctg gcc	288

Tyr	Lys	Lys	Leu	Arg	Asn	Leu	Thr	Asn	Leu	Leu	Ile	Ala	Asn	Leu	Ala	
				85					90					95		
atc	tcc	gac	ttc	ctg	gtg	gcc	atc	atc	tgc	tgc	ccc	ttt	gag	atg	gac	336
Ile	Ser	Asp	Phe	Leu	Val	Ala	Ile	Ile	Cys	Cys	Pro	Phe	Glu	Met	Asp	
			100					105					110			
tac	tat	gtg	gtc	cgg	cag	ctc	tcc	tgg	gag	cat	ggc	cac	gtg	ctc	tgt	384
Tyr	Tyr	Val	Val	Arg	Gln	Leu	Ser	Trp	Glu	His	Gly	His	Val	Leu	Cys	
		115					120					125				
gcc	tct	gtc	aac	tac	ctg	cgc	acc	gtc	tcc	ctc	tac	gtc	tcc	acc	aat	432
Ala	Ser	Val	Asn	Tyr	Leu	Arg	Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn	
	130					135					140					
gcc	ttg	ctg	gcc	atc	gcc	att	gac	aga	tat	ctc	gcc	att	gtt	cac	ccc	480
Ala	Leu	Leu	Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro	
145					150					155					160	
ttg	aaa	cca	agg	atg	aat	tat	caa	acg	gcc	tcc	ttc	ctg	atc	gcc	ttg	528
Leu	Lys	Pro	Arg	Met	Asn	Tyr	Gln	Thr	Ala	Ser	Phe	Leu	Ile	Ala	Leu	
				165					170					175		
gtc	tgg	atg	gta	tcc	att	ctc	att	gcc	atc	cca	tca	gcc	tac	ttt	gca	576
Val	Trp	Met	Val	Ser	Ile	Leu	Ile	Ala	Ile	Pro	Ser	Ala	Tyr	Phe	Ala	
			180					185					190			
aca	gaa	acc	gtc	ctc	ttt	att	gtc	aag	agc	cag	gag	aag	atc	ttc	tgt	624
Thr	Glu	Thr	Val	Leu	Phe	Ile	Val	Lys	Ser	Gln	Glu	Lys	Ile	Phe	Cys	
		195					200					205				
ggc	cag	atc	tgg	ccc	gtg	gat	cag	cag	ctc	tac	tac	aag	tcc	tac	ttc	672
Gly	Gln	Ile	Trp	Pro	Val	Asp	Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe	
	210					215					220					
ctc	ttc	atc	ttt	ggc	gtg	gag	ttc	gtg	ggc	cct	gtg	gtc	acc	atg	acc	720
Leu	Phe	Ile	Phe	Gly	Val	Glu	Phe	Val	Gly	Pro	Val	Val	Thr	Met	Thr	
225					230				235						240	
ctg	tgc	tac	gcc	agg	att	tcc	cag	gag	ctc	tgg	ttc	aag	gca	gtc	cct	768
Leu	Cys	Tyr	Ala	Arg	Ile	Ser	Gln	Glu	Leu	Trp	Phe	Lys	Ala	Val	Pro	
			245					250					255			
ggg	ttc	cag	aca	gag	cag	atc	cgt	aag	cgg	ctg	cgc	tgc	cgc	agg	aag	816
Gly	Phe	Gln	Thr	Glu	Gln	Ile	Arg	Lys	Arg	Leu	Arg	Cys	Arg	Arg	Lys	
		260					265					270				
aca	gtc	ctg	gtg	ctc	atg	tgc	atc	ctc	atg	gcc	tac	gtg	cta	tgc	tgg	864
Thr	Val	Leu	Val	Leu	Met	Cys	Ile	Leu	Met	Ala	Tyr	Val	Leu	Cys	Trp	
		275					280					285				
gca	ccc	ttc	tat	ggc	ttc	acc	atc	gta	cgc	gac	ttc	ttc	ccc	acc	gtg	912
Ala	Pro	Phe	Tyr	Gly	Phe	Thr	Ile	Val	Arg	Asp	Phe	Phe	Pro	Thr	Val	

290	295	300	
ttc gta aag gaa aag cac tac ctc act gcc ttc tac gtg gtc gag tgc			960
Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Val Val Glu Cys			
305	310	315	320
atc gcc atg agc aac agc atg atc aac acc gtg tgc ttc gtg acg gtc			1008
Ile Ala Met Ser Asn Ser Met Ile Asn Thr Val Cys Phe Val Thr Val			
	325	330	335
aag aac aac acc atg aag tat ttc aag aag atg atg ctg ctg cac tgg			1056
Lys Asn Asn Thr Met Lys Tyr Phe Lys Lys Met Met Leu Leu His Trp			
	340	345	350
cgt ccc tcc cag cgg ggg agc aag tcc agt gcc gac ctt gac ctt aag			1104
Arg Pro Ser Gln Arg Gly Ser Lys Ser Ser Ala Asp Leu Asp Leu Lys			
	355	360	365
acg aac ggg gtg cct gcc acg gaa gag gtg gac tgt atc agg ctg aag			1152
Thr Asn Gly Val Pro Ala Thr Glu Glu Val Asp Cys Ile Arg Leu Lys			
	370	375	380
tga			1155
*			

<210> 38  
 <211> 384  
 <212> PRT  
 <213> Saimiri sciureus

<400> 38

Met	Ala	Ala	Gln	Asn	Gly	Asn	Thr	Ser	Phe	Ala	Pro	Asn	Phe	Asn	Pro
1				5					10					15	
Pro	Gln	Asp	His	Ala	Ser	Ser	Leu	Ser	Phe	Asn	Phe	Ser	Tyr	Gly	Asp
			20					25					30		
Tyr	Asp	Leu	Pro	Met	Asp	Glu	Asp	Glu	Asp	Met	Thr	Lys	Thr	Arg	Thr
		35				40						45			
Phe	Phe	Ala	Ala	Lys	Ile	Val	Ile	Gly	Ile	Ala	Leu	Ala	Gly	Ile	Met
	50				55					60					
Leu	Val	Cys	Gly	Val	Gly	Asn	Phe	Val	Phe	Ile	Ala	Ala	Leu	Thr	Arg
65				70					75					80	
Tyr	Lys	Lys	Leu	Arg	Asn	Leu	Thr	Asn	Leu	Leu	Ile	Ala	Asn	Leu	Ala
			85					90					95		
Ile	Ser	Asp	Phe	Leu	Val	Ala	Ile	Ile	Cys	Cys	Pro	Phe	Glu	Met	Asp
		100					105					110			
Tyr	Tyr	Val	Val	Arg	Gln	Leu	Ser	Trp	Glu	His	Gly	His	Val	Leu	Cys
	115				120						125				
Ala	Ser	Val	Asn	Tyr	Leu	Arg	Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn
	130				135					140					
Ala	Leu	Leu	Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro
145				150					155					160	

Leu	Lys	Pro	Arg	Met	Asn	Tyr	Gln	Thr	Ala	Ser	Phe	Leu	Ile	Ala	Leu
				165					170					175	
Val	Trp	Met	Val	Ser	Ile	Leu	Ile	Ala	Ile	Pro	Ser	Ala	Tyr	Phe	Ala
			180					185					190		
Thr	Glu	Thr	Val	Leu	Phe	Ile	Val	Lys	Ser	Gln	Glu	Lys	Ile	Phe	Cys
		195					200					205			
Gly	Gln	Ile	Trp	Pro	Val	Asp	Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe
	210					215					220				
Leu	Phe	Ile	Phe	Gly	Val	Glu	Phe	Val	Gly	Pro	Val	Val	Thr	Met	Thr
225					230					235					240
Leu	Cys	Tyr	Ala	Arg	Ile	Ser	Gln	Glu	Leu	Trp	Phe	Lys	Ala	Val	Pro
			245						250					255	
Gly	Phe	Gln	Thr	Glu	Gln	Ile	Arg	Lys	Arg	Leu	Arg	Cys	Arg	Arg	Lys
			260					265					270		
Thr	Val	Leu	Val	Leu	Met	Cys	Ile	Leu	Met	Ala	Tyr	Val	Leu	Cys	Trp
		275					280					285			
Ala	Pro	Phe	Tyr	Gly	Phe	Thr	Ile	Val	Arg	Asp	Phe	Phe	Pro	Thr	Val
	290					295					300				
Phe	Val	Lys	Glu	Lys	His	Tyr	Leu	Thr	Ala	Phe	Tyr	Val	Val	Glu	Cys
305					310					315					320
Ile	Ala	Met	Ser	Asn	Ser	Met	Ile	Asn	Thr	Val	Cys	Phe	Val	Thr	Val
				325					330					335	
Lys	Asn	Asn	Thr	Met	Lys	Tyr	Phe	Lys	Lys	Met	Met	Leu	Leu	His	Trp
			340					345					350		
Arg	Pro	Ser	Gln	Arg	Gly	Ser	Lys	Ser	Ser	Ala	Asp	Leu	Asp	Leu	Lys
		355					360					365			
Thr	Asn	Gly	Val	Pro	Ala	Thr	Glu	Glu	Val	Asp	Cys	Ile	Arg	Leu	Lys
	370					375					380				

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<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic construct

<400> 39

Met Val Ile Thr Gly Ala

1

5